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PCT/NZ99/00107

SEQ ID NO: 1

GAATTCTTCTATGGCTATCACCATGTCCA	-10374
AAACACTACCTGAGTAAAGAAGGAGTCATTTTTTTTTTAAGGCTTTAAAA	-10324
AATTTAAAAATTTTAAATTAAATTTAAAAATGAAATCTAAAAAAATTTT	-10274
AAGAAAAATTTTTTTTAATCTGCAGAAACATACTCTGTATTGAGTCTATG	-10224
GTTACCAAAGATCCCCCAGAACAAAACCCCAAGAATTGCAAGATTTTCT	-10174
CTTGGAAGTGTTTGTCTTACTGGAAGGCTTATTAAGTCAATAATAAGGGA	-10124
GAGTAAAGACTTCAAACTAAAGATCTGTTTTTGTGAGTTCAATCTATAT	-10074
TGTCATCTGCTCTGGAAACCCTGAGCTTGTTCTAAAGTAACTGAACTAT	-10024
CATGAAGAAAATCAGCCATCAAAATAGTGAAAACGAACCTCTTACACTCA	-9974
GTTTTTCTCATTTGTAAATTTAAAAAATTTAACTTCATTAAGTCTGGGG	-9924
ACCAATGTATAGCTGCAAGCAGGAATTTTATGCCTTCTTAATCCAGAGAG	-9874
GTGGGCAATGGTGTGGGTTTAGACCAGAAGTAAGGATGTGGGTGCAGCAA	-9824
ATATGACAGCCCAACTGCTGCTGCTGCTGCTAAGTCACTTCAGTCGTGTC	-9774
CGACTCTGTGTGACCCAGAGACGGCAGCCACCAGGCTCCCCCGTCCCT	-9724
GGGATTCTCCAGGCAAGAACAACACTGGAGTGGGTTGCCATTTCTTCTCCAA	-9674
TGCATGAAAGTGAAAAGTGAAAGTGAAGTCGCTCAGTCGTGTCGACCCCT	-9624
CAGTGACCCCATGGACTGCAGCCTACCAGGCTTCTCCGTCCATGGGATTT	-9574
TCCAGGCAAGAGTACTGGAGTGGGGTGCCATTGCCTTCTCCATGACAGCC	-9524
CAACTAGAGACTGCTATAACTTATATCAGAGAATCTGAAACTCCCTACAG	-9474
GCTATCTTGCTATATGTGCATTCAACATGAACAAAAAGAAAATTCAAGTC	-9424
CAGTAAAAAGGGCTAAAATAGTGAATCACAGACTTTTGCCAAACAACAGT	-9374
CAATGATTTGGGCAAAGGACTTAAGTAGCTATGCTTATTTGCTATTAGTA	-9324
GAATAAAGAAATGTTTGAGCCTGGTTCTCAATGCTTGAATAATAAGATTC	-9274
CTTTTCAAGGAAAAACAATTTTTTTTGAGAACTCATAGATAAAAGTCAAAT	-9224
CTATCACTTTAGATGTCACTTGAAGCCAACTTGATTATAGTAAACAAATT	-9174
CAGCTGTAAACATTTTTTTTATAACACTGTAGACACTGTATTTTTATACAC	-9124
TGTATAAATGAAGACACTGAAGATGTAAAGTGGTGACCTGGATGATCCAG	-9074

Fig 1

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AATATGCAATATGCACCAAAAACTAAGTTTTTTAAATGATACAAATGAAC	-9024
TTACTTACAAAAGGGAAATAGAGTCACAGATGTAGAAAACATACAGTTAC	-8974
CTAGGGGGACGGGGGGAGGGTAAACTGGGAGATAGGAATTGACACATACA	-8924
CTCTACTATATATACACTAGGTAACCTAATATGAACCTACTGTATAGCGCA	-8874
CAGAACTCTACCCAATACTCTGTAATGACATTTATGGGAATAGAATCCAA	-8824
AAAGAGCAGATATGTGTATATGTATAAACTGATTCACACCCCTTGCCTTG	-8774
CCTAAACACACACAGACACACACAGACACATCCATTTTGAGATTTCTTTC	-8724
CTCCTCTTTGGCTACTTTTGACTCAGTTTGACCTAGATAGGACCTGTGCT	-8674
GGGTAAGGGCTTTGGCAGTCTTAAGTAGTGTGAGAGCAAGCACAGTCACT	-8624
CCCTAGCAAGGTCTTATTACTAGCTACAGAGTCTCTCTGTGCAGTCATAG	-8574
ATCACTGAGTGCAAAAGTCCAGTGCAATGTTTGAGTCCCATGCATGCTCT	-8524
CACAGAACTGAGAGAGGAGGCAAGGACACAGGACCCTCCAGTGCTGGGAC	-8474
TCTCTACTGGGGTGAGCAAGAGGGAACCCAATAGAAATGCTGCGAACCAC	-8424
AGAGCCACTCAGAAAGCCTGTAAATATAAACATAACAACACATTATGAAT	-8374
ATATAAGTATAAGTATACCTACCAAAAAATCAGAAAGTTGAACTTTTTTG	-8324
TATTCAAGGGAACAGTCATTCATTTATCGGTTTCAGTTATCAGTAAACACA	-8274
TTTGGGAACTGTAAAAATCTAATCAGTTCAGTTCAGTTCAGTCGCTCAGT	-8224
CGTGTCTCTTTGCGACTCCATGAATCGCAGCACGCCAGGCCTCCCTGTCT	-8174
ATCACCAACTCCCGGCGTTCACTCAGACTTACGTCCATCGAGTCAGTGAT	-8124
GCCATCCAGCCATCTCATCCTCTGTCTGTCCTCCCTTCTCCTCCTGCCCCAA	-8074
TCCCTCCCAGCATCAGAGTCTTTTCCAATGAGTCAACTCTTCTCACGAGG	-8024
TGGCCAAAGTACCAAGTCTTTGAGTCTAGTCTCTTTTTTCAATGGAGAAG	-7974
AAGAGGAAACCAAATTATAACTTAATTTTTATTCTTTGTATTACAAGTGT	-7924
ATAATTAATACACTGGAGTTTCCATTTTCAGAAAGGAAGAAGAGAAATCAC	-7874
ATTTTGCAGCTTTCCTGAACTAATAACAAAGAAATGCAGAAGTTTGTAA	-7824
CTGGGATATTATTATGACACGTTGCCATAATATGAATGTCATCATCTCAA	-7774
GACTGACCTGAAAACCAAAATAAAAAAAAAAAGAGAGAGAGAGAGAGA	-7724

Fig 1 contd

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GAGAGAAAAAAAGAAAACCCTCCAGACCAGATTTTCAGTCTACCACTTGA -7674
GCTGACAAACATTGGCCAAATGTCCTCTACAGAACCTGTAAGTTAGTAGT -7624
TGGTAATTATAAAACAATAAAGTATATATTTCTGCTCCTGGCAATAATTA -7574
TGTATCAGTTAAAAAGTATACATTGTCTAAAAAATCACCATATTTGATGT -7524
CTCATTAAAACAAAGTTACAAATATTAAGATGAGAGGACTTAAAGTTAGA -7474
TGGGAAAATATTCAATTGAAGCAGTATAAAATGCATTACTCTGGGGCAAA -7424
GTGTGGTCTGGAGATCCCTGGAGTGAAGACCCTTTTAGACAATCTGTGGA -7374
GTAAGAACTGTTTTTCATAACAAAGCTAAGATTTCCCTTGCTATTCTCATTT -7324
TCTCTTACGTATATAGTCGAGTTTTCCAGAAGTTCCATGTTATGTAACAT -7274
CATCATTTACTCTGTCAGCAAATAGAATACATGTTTGCATATGTCTATATT -7224
CTAACATTTCTCATTTTTTAATTTATAATTCATTAAATATTGATAGATATG -7174
ACCCACATAAAACAAAAGCTTTTCAGGATCCTGAATAACTTTTCAGAGTAA -7124
AGGAATCTTGAGACCAAAGGTTTGAGAATTACTGTTTTAGGGGATACAC -7074
CTCAAGTGAAAGAGCACGCCTCATCACATTTCCACTCTATATGGAAGAAT -7024
CTAGAAGATTGAACCTATAATTGAAGAGTGCAGGCTTTATGAAGACAGTG -6974
ACTGTTTCTGTCTGCTTTCTCCTCAGAATTTAGCATGATGCCAGGCACAT -6924
AATTTGTTGTTGTTTCAGCTGCTAAGTCATCTCTGACTTTTTTGCAACCCCA -6874
TGAAGTGCATGCAACATGCCAGGTTTCTCTGCTTTCACTATCTCCTGGAG -6824
TTTGCTCCAACTCATGTCCATTGAGTCACTGATACCATCCAACGATCTCA -6774
TCCTCTATAAGACACATTATAGACATTAGAATATTTTCATAAAATAATAA -6724
GTGAATTAATACAGCTGAAACTCAAACAGCATAGGGGTACAAAGTACCAA -6674
CTCGCGTCCAAGTTGAAAATCCACATATAATCTTAAGGTCAGCCTTGAT -6624
ACATGCATATCCAAGGTTCCCCATCTGAGGATTCAACCAACCTCAGATAG -6574
TGTAAGTACTGCAGTACACATTTAGTGAAAAATGTGCATATAAGTGGACCC -6524
ATGCAGGTCAAACCTGCGTTTTTCCAAGGGTCCACAGTACACACACACATG -6474
CATACATGCATCTCTAAATGAAAGCTTTGCCATCTGACTTACTCAAGGTC -6424
ACATAAAACGTCAGCGAGAAACCCAGAACTATATTCAGATCTCTGTTCC -6374

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TATACTGTTACTCCCTGAGTCAAGGGTACTTTTGTGTTTGTTCATTTTTTA	-6324
TTCTGTAATCTATTGAGATCACAGATAATCAGATGTTGCCACTGTAGGAT	-6274
GGCAGCCTCTCATGCTGTTATGTGAATTGAGCACTATCCAGTTTGTGTTCT	-6224
GGCTTTAAGTGTAATCAGAACAGTGTTATATCAAAGGGCTATCATCACAA	-6174
GGAAATGGCAAGAGTGATCAGATAAAATGCATCTTTCTCTCTTTTCCCAC	-6124
AACAGACTCGAATTTTTTCATGATTTCATCCTTATTCTAATTCTTCAGTTCA	-6074
GTTTCAGTTTCAGTCCTTCAGTCATGTCCAACCTTTTGCCACCCCATGAATC	-6024
TCAGCAAGCCAGGCCTCCCTGGTCCATCACCAACTCCCAGAGTTCACCCA	-5974
GACTCACGTCCATCGAGTCAGTGATGCCATCTAGCCATCTCATCCTCTGT	-5924
CGTCCCCCTTCTCTTCCTGCCCCCAATCCCTCCCAGCATCAGAGTCTTTTC	-5874
CAATGAGTCAACTTTTCACATGAGGTGGCCAAAGTACTGGAGTTTCAGCT	-5824
TTAGCATCATTCCTTCCAAAGAAATCCCAGGGCTGATCTCCTTCAGAATG	-5774
GACTGGTTGGATCTCCTTGCAGTCCAAGGGACTCTCAAGAGTCTTCTCCA	-5724
ACACCACAGTTCAAAAGCATCAATTCTTCGGCGCTCAGCTTTCTTCACAG	-5674
TCCAACCTCTCACATCCATACATGACCACAGGAAAAACCATAGCCTTGACT	-5624
AGATGGACCTTTGTTGGCAAAGTAATGTCTCTGCTTTTCAATATGCTATC	-5574
TAGGTTGGTCATAACTTTCCTTCCAAGGAGTAAGCATCTTTTAATTTTCAT	-5524
GGCTGCAGTCACCATTTGTAGTGATTTTGGAGCCCAGAAAAATAAAGTCT	-5474
TGACACTGTTTCCACTGTTTCCCCATCTTATTTCCCATGCAGTGATGGGA	-5424
CCGGATGCCATGATCTTAGTTTTCTGAATGTTGAGCTTTAAGCCAACTTT	-5374
TTCAATCTCCTCTTTCACTTTCATCAAGAGGCTTTTGAGTTCCTCTTCAC	-5324
TTTCTGCCATAAGGGTGGTGTCATCTGCATATCTGAGGTTATTAATATTT	-5274
CTCCCGGCAATCTTGATTCCAGCTTGTGCTTCTTCCAGCCCAGTGTGTTCT	-5224
CATGATGTACTCTGCATAGAAGTTAAATAAGCAGGGTGACAATATACAGT	-5174
CTTGACATCCTCCTTTTCCTATTTGGAACCAGTCTGTTGTTCCATGTCCA	-5124
GTTCTAACTGTTGCTTCCTGACCTGCATACAGGTTTCTCAAGAGGCAGGT	-5074
CAGGTGGCAGGTCAGGTGGTCAGGAACATCTCTTTCAGAATTTTGGACAG	-5024

Fig 1 contd

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TTTATTGTGATCCACACAGTCAAAGGCTTTGGCATAGTCAATAAAGCAGA	-4974
AATAGATGTTTTTCTGGAACCTCTCTTGCTTTTTTCGATGATCCAGCAGATG	-4924
TTGGCAATTGATCTCTGGTTCCTCTGCCTTTTCTAAAACCAGCTTGAAC	-4874
ATCAGGAAGTTCATGGTTCACGTATTGCTGAAGCCTGGCTTGGAGAATTT	-4824
AGAGCATTACTTTACTAGCATTACTTTTCACAATAAACTGTGGAAAATTC	-4774
TGAAAGAGATGGGCATACCAGACCACCGGATCTGCCTCTTGAGAAATTTG	-4724
CATGCAGGTCAGGAAGCAACAATTAGAAGTGGACATGGAACAACAGACTG	-4674
GTTCCAAATAGGAAAAGGTGTTTCGTCAAGGCTGTATATTGTCACCCTGTT	-4624
TATTTAACTTCTATGCAGAGTACATCATGAGAAACGCTGGGCTGGAAGAA	-4574
GCACAAGCTGGAATCAAGATTTCCGGGAGAAATATCAATAACCTCAGATA	-4524
TGCAGATGACACCACCCTTATGGCAGAAAGTGCAGAGGAACTAAAAAGCC	-4474
CCTTGATGAAAGTGAAAGTGGAGAGTGAAAAAGTTGGCTTAAATCTCAAC	-4424
ATTCAGAAAACGAAGATCATGGCATCCGGTCCCATCACTTCATGGGAAAT	-4374
AGATGGGGAAACAGTGGAACAGTGTGAGACTTTATTTTTCTGGGCTCCA	-4324
AAATCACTACAAATGGTGACTGCAGCCATGAAATTAAAGATGCTTACTC	-4274
CTTGGAAGGAAAGTTATGACCAACCTAGATAGCATATTGAAAAGCAGAGA	-4224
CATTACTTTGCTAACAAAGGTCCATCTAGTCAAGGCTATGGTTTTTCCTG	-4174
TGGTCATGTATGGATGTGAGAGTTGGACTGTGAAGAAAGCTGAGTGCCGA	-4124
AGAATTGATGCTTTTGAACTGTGGTGTGAGAGAAAGACTCTTGAGAGTCCC	-4074
TTGGACTGCAAGGAGATCCAACCAGTCCATTCTGAAGGAGATCAGCCCTG	-4024
GGATTTCTTTGGAAGGAATGATGCTAAAGCTGAAACTCCAGTACTTTGGC	-3974
CACCTCATGTGAAGAGCTGACTCATTTGAAAAGACTCTGATGCTGGGAGG	-3924
GATTGGGGGCAGGAGGAGAAGGGGGCGACAGAGGATGAGATGGCTGGATG	-3874
GCATCACTGACTCAATGGACGTGAGTCTGTGTGAACTCTGGGAGTTGGTG	-3824
ATGGACAGGGAGGCCTGGCGTGCTTTGATTCATGGGGTCACAAAGAGTCG	-3774
GACACGACTGAGCGACTGATCTGTCTCTCTTACTAGCATGTGTCTCCT	-3724
CCTTTTTTTGCCACATCATCAAACCTCTGGCAAACCTCACATTAATAACA	-3674

Fig 1 contd

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TTTGGGAGCTTCCAGAATGCAAACAGTGAAACCATTAATGTTTTTTGGGA	-3624
AATATGCTTTTATACTCTCAATGTTGTTTTGAAACGCACACCCCCCTCCCCT	-3574
GCCGCCTGGTGTGTTGTAAGACAGTTGAGAGAAGTTTGCTTGCTACCTTAC	-3524
TTATGGTTACACAAACGTAAGGCCCCCTGAGTACAAAGAAGAACAGGGGG	-3474
AACGCAAACCTTCAGGCCCTGTGAGGAGGGGCACTGGACTCCTGTGAGAAG	-3424
AAACTGCTTTCAAAGAATTCCTGGGAGAAATTCTCTATGCACTCATCCTA	-3374
GCAACAAAGTCCTGTCCGAAGTTAGGCCCGCAGCACCCACACGGCAGTGA	-3324
AGGTTCCCTACTGCTGGTGAACCTTGCTGCTCCGAAGCCATAGGAAGGTTG	-3274
CAAATCCCGGCACTGGAGAAGGAAAACACGTTCTTGAAATTTCTTGAGTA	-3224
CCTCTTAATTCATTCAATGCTGACCTCCGGAGATTGGATAGAGCTGACTC	-3174
TCATTATTCACAGTGGTTATGTTCTACCCAATCACTGCCAACATGAATAA	-3124
GTGATTCCCTGAACCACTGCCCCCTAGGGGAACTACAAGGTTAGATTCCCGT	-3074
CAGCCTCTGGTCACGTTTTTTGTTAACCAATCAATAAATAACCTTGTTTTG	-3024
TGTGCATTTCTGTTTTTAAAATATCTTTATTTAATACGTACTGCTAATTCT	-2974
TCAACATTTGGTTCACAACCAAAAAGGCCCTATTAAGTGAAGCCCTGAAT	-2924
GAAGCTTACATAACACACATTGTTTTTCTATGAGGAAAAATTTTTTCCTTC	-2874
AGTCCTGCCACAGCCTTCTTGCTTAAAATTGTGGACAAAATATACATAAC	-2824
ATGAAACTGACTATTATTTAACTGATTTTAACTGTACAGTTCAGTGGCAT	-2774
TAAGTACACTTACCTTGCTGTGGAACCTATGATCAACATTCATCTCTAGAA	-2724
CTTTTTGATCTTCTCGAATTGAAAACCTCTGCATCTATTGCACAGTAGCTT	-2674
TCCCCCATCACACCGCACCCCTTCCTCCAGCCCCCGGCACCACCATCCTT	-2624
CTTTCCATGACAGTCATCCTGTGCCTAGGAACACAGCCCTTCAACACTAC	-2574
GCTTGGGGGGCACTGTAAGCAACAGGATCACTCCCTACCGCCACCAAATG	-2524
CACACAAAAATATAAAAAGCATGGTGGCATATCGATTGCAAAAAGGGTGC	-2474
TTGCTAAGTATGAGGGCTGAAACAAGGCAGAGAATTGACTAGGTTGACCT	-2424
CAGCTGGGATCCTGTGTGTTGGAAGCCTCAAATTTTCCATTGTTCTGTGC	-2374
ATACGCACAAATGCTTATAAAAAGCACTGTAAGGATTGATTATGAAGTTAA	-2324

Fig 1 contd

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GATAAATCTCAGCAAGACATAAATGTGCAAGCACGGGATCCATGAATAAC -2274
 GAGCACTGACCATGTGGAAATGATAATCTTTGTTTCCTTTATTCCAGGCA -2224
 GTAAGGAGAAAGCGCTCACAGGGCTGCCTTACACCATTTTACTAGAGAGC -2174
 TAGCCTATGTCAGTCGGTAGCTGGCAATTACAAACTGAAGCAGTTCTAGT -2124
 TCATGTGGAGGATGAATTTAACCATAATCTCAACCCCTCTGCATGAAAC -2074
 AGAGACTAAGTACTCAAGTACCAGTTATCAGTCACTTACTATATGACAGG -2024
 CACTGTACTCAACAATTTACATGTATTATTGAATTACATGCCCCAACAC -1974
 TCTATGAGGAAGCTGAAGGTTAGAGAAGTATCTCATTATTATTACACAG -1924
 TGGCAAACTGAGATCTGAACTCAGGTCTATCCAACCTCAGGACCTGAGAT -1874
 CCCAATTGCTACACAATTCTAATCAAGTTAAAAGGGAAAAAGGATTTGAT -1824
 TTGCTCAGAAGTGTATAGGGGCATATGTTACAATTATAACATTACAAAGA -1774
 TTTATATGTTGAAAAATAAATTTATCAAACAAATAAACTTTATAAGCCT -1724
 GATCTAATACTGCTCCGCAACAAAGACTATCTGAAATCCTTCAGGGCATC -1674
 TGGTTTGTGTCTGGTTTTCTTAATCTTTAATGATGGGCAAATCTAATGC -1624
 ATTATGTAAGGCCATTTTTTCTCAAGAGATGTAGATACCTCTTAAGAATT -1574
 TGATGAAAATGCATTAACCTTTTCAGGCTACTGAGTTGCATTTTAGTGCAC -1524
 TGAGGCAGTAAATTAGTGTACAATGTGCGAAAGTAGTGACCTAAAAAATA -1474
 AATATTTGATATGAACCACTGCACTCTCTTGGGGAAAAAAGTAATGGATT -1424
 AACTCTCTTAGGAGTCCTTAGCTTCCCCAAAAGTAGTAGGAAAAATAAAT -1374
 CTCCTGTGGCCTGGAAACAGCTTCTGTTTCTTGCTGGCTATATTTGTTTA -1324
 GGTTTTTAATAGTT**CATTTG**ATTAGACCTTGTGGCTCCCAAAGCTAAGGT -1274

E-box (4)

TGAGAGTTTGATCCCTACAGAGGCCACTTCAATTTAGAGAACAAAAAGCC -1224
 CCATTCTCTGCTCCCAGACCTTACCCCAAATCCCTGCCAGGTGTCTGCCC -1174
 TCCGGT**CA**AATGAGAACTGGCAAAGGAAGTACTAGGAGGTGCACAGTA -1124

E-box (3)

CTAGGAAGTAGAAAAATGGACTAGCACACTACTGAGAAGCAGAAAAATGG -1074

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GCACCCTTCATGATGGTGTTCCTTTCCCTTTCTGTGTTCACAATGCTCCG -1024
 ATATAATTTACAGAGGGTAGATAACTACATTTTTTTCTTTTACCACTGGA -974
 AGGCTGAGGAAACTTTGTTACCCATCATAAAATTCACATCTTCTAAGT -924
 CATTCTATGTTATTCTAAGATCAAATAGCTGACAATATCCTCTTTGTAAT -874
 AAACAATGAAAAACACATCCTCTGAGCAATATTAATCTGCAACTTTAGG -824
 ATAGGAAGTAACTTAATACTAGTCAATTGAACTGAAATACAATTTTCAT -774
 ATGAATAAAAGATATTATTTAAAGTAATTCCATGAGCAATTTAATATTA -724
 AAGTAGGATTTTCATTATGTGTTAAGAATTTATTCAGGGAAACAAGTTTC -674
 TCAAATTATAGCAGAAAATCTTTTACTAGTATCACAGTCTTTTCATTTAA -624
 GTCTTCCTGAATAAATCTGTATTTTCTAATTATACAAGACTAAAAATAAT -574
 MEF2-site
 TTAATATAACAAATAAAATTATTTTTACTTCAAATGCTTACTTAAATAGT -524
 E-box (2)
 ATAAATCATTTTATTTTCTGAGGGAAAAGCATATCAACTTTTTAAGTAT -474
 TATA-box (3)
 GAAGTGTAATTAAGATTTATTCACTTAAATTATAATTTTTTAAAGTTTCA -424
 CATATAAAGATGAATAAGATCTAAGTGTATATGTTATTGTTAATAAAGTT -374
 TTTAATTTTTCGCATGTCACATACAGCCTTTATTATTCATAGATTTATTC -324
 CTTTTAAGAAGTAGTCAAATGAATCAGCTCACCTTGACTGTAACAAAAT -274
 E-box (1)
 ACTGTTTGGTGACTTGTGACAGACAGGGTTTTAACCTCTGACAGCGAGAT -224
 TCATTGTGGAGCAAGAGCCAATCACAGATCCCGACGACACTTGTCTCATC -174
 CAAT-box
 AAAGTTGGAATATAAAAAGCCACTTGGAATACAGTATAAAAGATTCACTG -124
 TATA-box (2) TATA-box (1)
 GTGTGGCAAGTTGTCTCTCAGACTGGGCAGGCATTAACGTTTGGCTTGGC -74
 GTTACTCAAAAGCAAAAGAAAAGTAAAAGGAAGAAGTAAGAACAAGGGAA -24

Fig 1 contd

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AAGATTGTATTGATTTTAAACCATGCAAAACTGCAAATCTCTGTTTAT +27
ATTTACCTATTTATGCTGATTGTTGCTGGCCCAGTGGATCTGAATGAGAA +77
CAGCGAGCAGAAG +90

FIG. 1. Nucleotide sequence of the 10,492-basepair promoter-enhancer region of bovine myostatin. Total length of the DNA sequence is 10,492 basepairs (bps) which consist of 10,402 bps of upstream and 90 bps of coding sequence. The coding sequence of myostatin is underlined. Nucleotides and the relative position of putative nucleotide motifs are numbered with respect to the translation start site (+1 bp). Consensus sequences for basic functional elements of a mammalian promoter (TATA and CAAT boxes) and for known muscle specific transcription factors (E-box and MEF2 sites) are bolded in the sequence and they are listed below.

TATA-boxes[1]: -139 bps(1); -163 bps(2);
 -524 bps(3)
 CAAT-box[2]: -206 bps
 E-boxes[3]: -308 bps(1); -543 bps(2)
 -1167 bps(3); -1309 bps(4)
 MEF2 site[4]: -584 bps

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Myostatin Promoter Activity

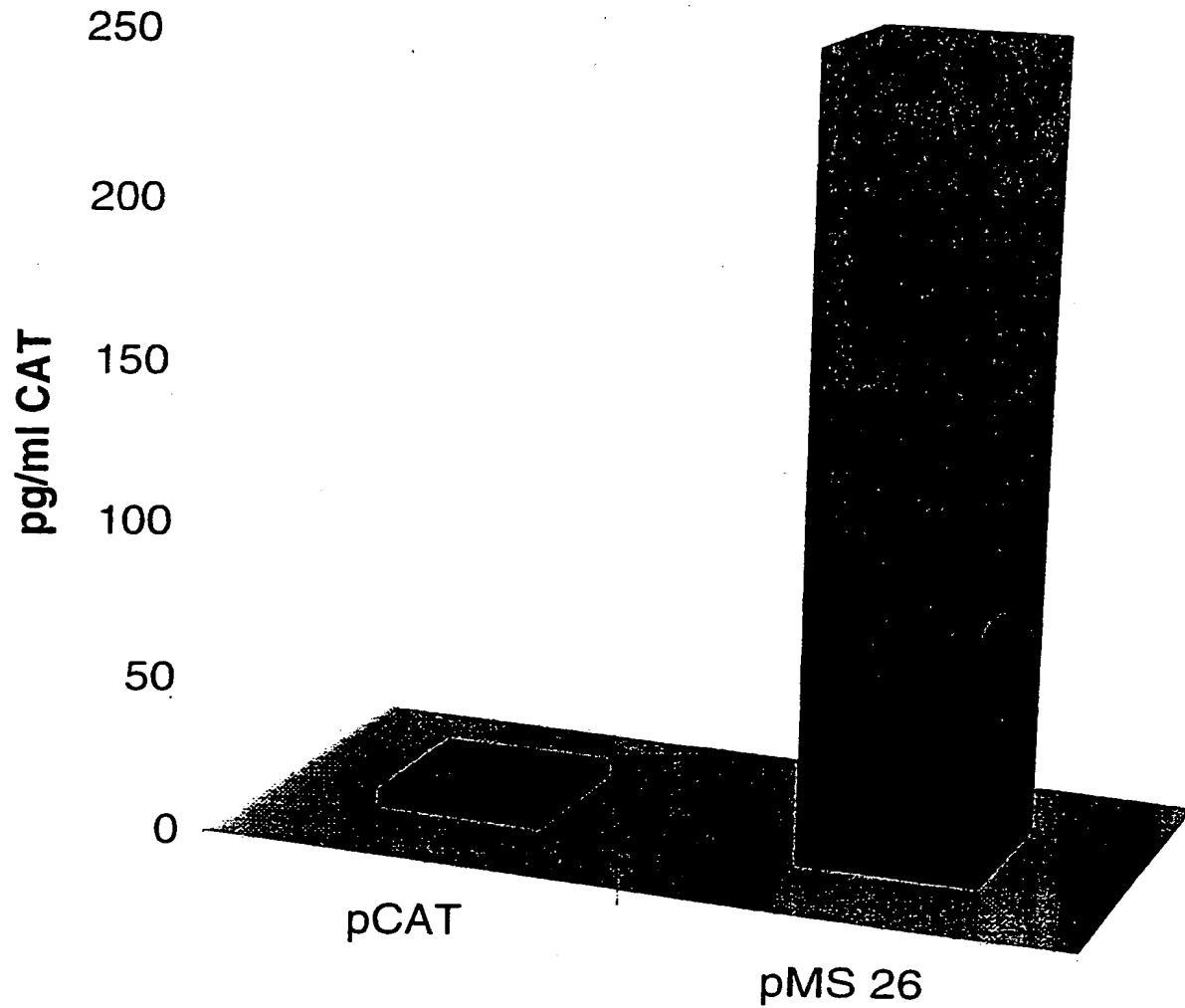


Fig 2